SEQUENCE LISTING

<110> Eberhard Hildt, Prof. Hofschneider

<120> Particles for Gene Therapy

<130> 319-2 US

<140> PCT/DE00/00363
<141> 2000-02-04

<150> DE 199 04 800.2
<151> 1999-02-05

<160> 19

<170> PatentIn Ver. 2.1

<210> 1
<211> 347
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      Fusion protein comprising a LHBs and heterologous binding site
      RGD

<400> 1

    Met Gly Arg Gly Asp Gly Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro
    1   5   10   15

    Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu
                20   25   30

    Glu Thr Leu Pro Ala Asn Pro Pro Ala Ser Thr Asn Arg Gln Ser
            35   40   45

    Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu Arg Asn Thr His Pro
        50   55   60

    Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp
    65   70   75   80

    Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly
                85   90   95

    Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe
                100   105   110

    Ser Arg Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly
            115   120   125

    Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr
        130   135   140

    Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu
    145   150   155   160

    Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser

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                        165                170                175
      Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly
                  180                185                190

      Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu
              195                200                205

      Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met
          210                215                220

      Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly
      225                230                235                240

      Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro
                  245                250                255

      Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro
                  260                265                270

      Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser
              275                280                285

      Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
          290                295                300

      Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp
      305                310                315                320

      Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu
                  325                330                335

      Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
                  340                345
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<210> 2
<211> 215
<212> PRT
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Fusion protein comprising a HBcAg, a cell-permeability-
          mediating polypeptide and heterologous binding site RGD

<400> 2

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      Met Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Thr Val Gln
      1               5                10                15

      Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile Asp Pro
                  20                25                30

      Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
              35                40                45

      Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
          50                55                60

      Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
      65                70                75                80

      Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
                  85                90                95
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Thr Trp Val Gly Val Asn Leu Glu Asp Pro Glu Phe Arg Gly Asp Ala
            100                 105                 110

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
        115                 120                 125

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
    130                 135                 140

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
145                 150                 155                 160

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
                165                 170                 175

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
            180                 185                 190

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
            195                 200                 205

Gln Ser Arg Glu Pro Gln Cys
    210                 215
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<210> 3
<211> 663
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      DNA coding for a fusion protein comprising a HBcAg, a cell-
      permeability-mediating polypeptide and heterologous binding
      site RGD

<400> 3

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atgcccatat cgtcaatctt ctcgaggatt ggggaccctg gatccactac tgttcaagcc    60

tccaagctgt gccttgggtg gctttggggc atggacatcg acccttataa agaatttgga    120

gctactgtgg agttactctc gtttttgcct tctgacttct ttccttcagt acgagatctt    180

ctagataccg cctcagctct gtatcgggaa gccttagagt ctcctgagca ttgttcacct    240

caccatactg cactcaggca agcaattctt tgctgggggg aactaatgac tctagctacc    300

tgggtgggtg ttaatttgga agatccagaa ttccgaggcg acgcgtctag agacctagta    360

gtcagttatg tcaacactaa tatgggccta aagttcaggc aactcttgtg gtttcacatt    420

tcttgtctca cttttggaag agaaaccgtt atagagtatt tggtgtcttt cggagtgtgg    480

attcgcactc ctccagctta tagaccacca aatgccccta tcctatcaac acttccggaa    540

actactgttg ttagacgacg aggcaggtcc cctagaagaa gaactccctc gcctcgcaga    600

cgaaggtctc aatcgccgcg tcgcagaaga tctcaatctc gggaacctca atgttagtat    660
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tcc   663

<210> 4
<211> 1047
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
        DNA coding for a fusion protein comprising a LHBs and
        heterologous binding site RGD

<400> 4

atgggccgtg gcgaaggagc tggagcattc gggctgggtt tcaccccacc gcacggaggc   60

cttttggggt ggagccctca ggctcagggc atactacaaa ctttgccagc aaatccgcct   120

cctgcctcca ccaatcgcca gacaggaagg cagcctacc cgctgtctcc acctttgaga   180

aacactcatc ctcaggccat gcagtggaat tccacaacct ttcaccaaac tctgcaagat   240

cccagagtga gaggcctgta tttccctgct ggtggctcca gttcaggagc agtaaaccct   300

gttccgacta ctgcctctcc cttatcgtca atcttctcga ggattgggga ccctgcgctg   360

aacatggaga acatcacatc aggattccta ggacccctc tcgtgttaca ggcggggttt   420

ttcttgttga caagaatcct cacaataccg cagagtctag actcgtggtg gacttctctc   480

aattttctag ggggaactac cgtgtgtctt ggccaaaatt cgcagtcccc aacctccaat   540

cactcaccaa cctcctgtcc tccaacttgt cctggttatc gctggatgtg tctgcggcgt   600

tttatcatct tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac   660

tatcaaggta tgttgcccgt ttgtcctcta attccaggat cctcaaccac cagcacggga   720

ccatgccgaa cctgcatgac tactgctcaa ggaacctcta tgtatccctc ctgttgctgt   780

accaaacctt cggacggaaa ttgcacctgt attcccatcc catcatcctg ggctttcgga   840

aaattcctat gggagtgggc ctcagcccgt ttctcctggc tcagtttact agtgccattt   900

gttcagtggt tcgtagggct ttcccccact gtttggcttt cagtatatg gatgatgtgg   960

tattgggggc caagtctgta cagcatcttg agtccctttt taccgctgtt accaatttc   1020

ttttgtcttt gggtatacat ttaaacc   1047

<210> 5
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
        Primer

<400> 5

ccatattctt gggaacaaga tatccagcac ggggc   35

<210> 6
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      Primer

<400> 6

ggattgctgg tggaagatat ctgccccgtg ctg   33

<210> 7
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      Primer

<400> 7

cagcacgggg cagatatctt ccaccagcaa tcc   33

<210> 8
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      Primer

<400> 8

gccccgtgct ggatatcatc ttgttcccaa gaatatgg   38

<210> 9
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
      Primer

<400> 9

aaaagatctg cccgtggcga agcagctgga gcattc   36

<210> 10
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
       Primer

<400> 10

aaaagatctg gtttaaatgt atacccaaag   30

<210> 11
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
       Primer

<400> 11

cccgatatca tgtcatctct tgttcatgtc cta   33

<210> 12
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
       Primer

<400> 12

ggggatatcg gtcgatgtcc atgccccaaa   30

<210> 13
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
       Primer

<400> 13

ggggatccc gatgtacggg ccagatatac gcgttg 36

<210> 14
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer

<400> 14

ggggatccg cggccgcttt acttgta 27

<210> 15
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer

<400> 15

nnnagatcta tgcccatatc gtcaatcttc tcgaggattg gggaccctgg atccnnn 57

<210> 16
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer

<400> 16

nnnggatcca ctgttcaagc ctccaagctg 30

<210> 17
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer

<400> 17

nnngaattct ggatcttcca aattaacacc caccca 36

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<210> 18
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer


<400> 18

nnngaattcc gaggcgacgc gtctagagac ctagtagtc                    39


<210> 19
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:
          Primer


<400> 19

nnnaagcttt ccccacctta tgagtccaag                              30
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